

SEQUENCE LISTING

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Fred Meins
Zhenya Glazov

<120> Methods of Controlling Gene Expression

<130> PB/5-31481A

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<170> PatentIn Ver. 2.1

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<212> DNA

<213> Arabidopsis thaliana

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Ser Ser Ser Ser Ser Ala Ala Pro Thr Val Gln Ala Thr Thr Ser Val

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His Gly His Glu Glu Asp Pro Asn Gln Ile Pro Asn Asn Ile Arg Arg
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Gln Leu Pro Arg Ser Ile Thr Ser Ser Thr Ser Tyr Lys Arg Phe Pro
65 70 75 80

Leu Ser Arg Cys Arg Ala Arg Asn Phe Pro Ala Met Arg Phe Gly Gly
85 90 95

Arg Ile Leu Tyr Ser Lys Thr Ala Thr Glu Val Asp Lys Arg Ala Met
100 105 110

Gln Leu Ile Lys Val Leu Asp Thr Lys Arg Asp Glu Ser Gly Ile Ala
115 120 125

Phe Val Gly Leu Asp Ile Glu Trp Arg Pro Ser Phe Arg Lys Gly Val
130 135 140

Leu Pro Gly Lys Val Ala Thr Val Gln Ile Cys Val Asp Ser Asn Tyr
145 150 155 160

Cys Asp Val Met His Ile Phe His Ser Gly Ile Pro Gln Ser Leu Gln
165 170 175

His Leu Ile Glu Asp Ser Thr Leu Val Lys Val Gly Ile Gly Ile Asp
180 185 190

Gly Asp Ser Val Lys Leu Phe His Asp Tyr Gly Val Ser Ile Lys Asp
195 200 205

Val Glu Asp Leu Ser Asp Leu Ala Asn Gln Lys Ile Gly Gly Asp Lys
210 215 220

Lys Trp Gly Leu Ala Ser Leu Thr Glu Thr Leu Val Cys Lys Glu Leu
225 230 235 240

Leu Lys Pro Asn Arg Ile Arg Leu Gly Asn Trp Glu Phe Tyr Pro Leu
245 250 255

Ser Lys Gln Gln Leu Gln Tyr Ala Ala Thr Asp Ala Tyr Ala Ser Trp
260 265 270

His Leu Tyr Lys Val Thr Thr Lys Asn His Leu Leu Thr Leu Asn
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<212> PRT

<213> Arabidopsis thaliana

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35 40 45

Thr Leu Thr Lys Pro Gln Glu Glu Tyr Lys Ile Leu Val Asp Asn Ala
50 55 60

Asn Asn Pro Phe Glu His Val Leu Leu Glu Lys Ser Glu Asp Gly Leu
65 70 75 80

Arg Phe Ile His Pro Leu Glu Glu Leu Ser Val Met Asp Phe Val Asp
85 90 95

Arg Asn Leu Ser Glu Met Arg Pro Val Lys Pro Leu Pro Leu Glu Glu
100 105 110

Thr Pro Phe Lys Leu Val Glu Glu Val Lys Asp Leu Glu Asp Leu Ala
115 120 125

Ala Ala Leu Gln Ser Val Glu Glu Phe Ala Val Asp Leu Glu His Asn
130 135 140

Gln Tyr Arg Thr Phe Gln Gly Leu Thr Cys Leu Met Gln Ile Ser Thr
145 150 155 160

Arg Thr Glu Asp Tyr Ile Val Asp Ile Phe Lys Leu Trp Asp His Ile
165 170 175

Gly Pro Tyr Leu Arg Glu Leu Phe Lys Asp Pro Lys Lys Lys Lys Val
180 185 190

Ile His Gly Ala Asp Arg Asp Ile Ile Trp Leu Gln Arg Asp Phe Gly
195 200 205

Ile Tyr Val Cys Asn Leu Phe Asp Thr Gly Gln Ala Ser Arg Val Leu
210 215 220

Lys Leu Glu Arg Asn Ser Leu Glu Phe Leu Leu Lys His Tyr Cys Gly
225 230 235 240

Val Ala Ala Asn Lys Glu Tyr Gln Lys Ala Asp Trp Arg Ile Arg Pro
245 250 255

Leu Pro Asp Val Met Lys Arg Tyr Ala Arg Glu Asp Thr His Tyr Leu
260 265 270

Leu Tyr Ile Tyr Asp Val Met Arg Met Glu Leu His Thr Met Ala Lys
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Glu Asp Glu Gln Ser Asp Ser Pro Leu Val Glu Val Tyr Lys Arg Ser
290 295 300

Tyr Asp Val Cys Met Gln Leu Tyr Glu Lys Glu Leu Trp Thr Arg Asp
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Ser Tyr Leu His Val Tyr Gly Val Gln Thr Gly Asn Leu Asn Ala Val
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Gln Leu Ser Ile Val Ala Leu Gln Gly Leu Cys Glu Trp Arg Asp Arg
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Ile Ala Arg Ala Asp Asp Glu Ser Thr Gly Tyr Val Leu Pro Asn Lys
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Arg Arg Leu Leu Lys Ser Lys Leu Pro Tyr Leu Glu Arg Asn Phe Asp
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Ala Val Ile Ser Val Ile Arg Arg Ser Met Gln Asn Ala Ala Ala Phe
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Glu Pro Val Val Gln Ser Leu Lys Asp Arg Arg Pro Glu Thr Val Val
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Glu Met Asn Ile Glu Pro Lys Ile Glu Lys Thr Asp Thr Gly Ala Ser
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Ala Ser Ser Leu Ser Leu Glu Lys Val Cys Val Asp Asp Ser Lys Lys
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Gln Ser Ser Gly Phe Gly Val Leu Pro Leu Lys Arg Lys Leu Glu Ser
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Asp Lys Thr Val Val Glu Lys Asn Ile Glu Pro Lys Ile Glu Lys Thr
485 490 495

Gly Thr Glu Ala Ser Ala Ser Ser Leu Ser Ser Lys Lys Val Cys Val
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Asp Asp Ser Lys Lys Gln Ser Ser Gly Phe Gly Val Leu Leu Ser Lys
515 520 525

Arg Lys Phe Glu Ser Asp Asn Lys Lys Leu Gln Val Lys Glu Glu Val
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Lys Val Ser Lys Ser Lys Pro Asp Lys Val Ile Ile Val Val Asp Asp
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565 570 575

Ala Asp Ala Leu Asp Arg Val Ser Glu Thr Pro Ser Lys Gly Ser Pro
580 585 590

Ser Leu Thr Gln Lys Pro Lys Thr Cys Asn Thr Glu Val Ile Val Leu
595 600 605

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610 615 620

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20 25 30

Leu Glu Asn Pro Gln Ile Glu Phe Gly Phe Leu Arg Gly Glu Cys Ser
35 40 45

Leu Glu Met Ser Asp Ser Tyr Val Trp Val Glu Thr Glu Ser Gln Leu
50 55 60

Lys Glu Leu Ala Glu Ile Leu Ala Lys Glu Gln Val Phe Ala Val Asp
65 70 75 80

Thr Glu Gln His Ser Leu Arg Ser Phe Leu Gly Phe Thr Ala Leu Ile
85 90 95

Gln Ile Ser Thr His Glu Glu Asp Phe Leu Val Asp Thr Ile Ala Leu
100 105 110

His Asp Val Met Ser Ile Leu Arg Pro Val Phe Ser Asp Pro Asn Ile
115 120 125

Cys Lys Val Phe His Gly Ala Asp Asn Asp Val Ile Trp Leu Gln Arg
130 135 140

Asp Phe His Ile Tyr Val Val Asn Met Phe Asp Thr Ala Lys Ala Cys
145 150 155 160

Glu Val Leu Ser Lys Pro Gln Arg Ser Leu Ala Tyr Leu Leu Glu Thr
165 170 175

Val Cys Gly Val Ala Thr Asn Lys Leu Leu Gln Arg Glu Asp Trp Arg
180 185 190

Gln Arg Pro Leu Ser Glu Glu Met Val Arg Tyr Ala Arg Thr Asp Ala
195 200 205

His Tyr Leu Leu Tyr Ile Ala Asp Ser Leu Thr Thr Glu Leu Lys Gln
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Leu Ala Thr Gly Arg His Leu Cys Tyr Gly Glu Thr Phe
225 230 235

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Tyr Ile Thr Lys Val Ile His Asp Cys Lys Arg Asp Ser Glu Ala Leu
35 40 45

Tyr Phe Gln Phe Gly Ile Arg Leu His Asn Val Val Asp Thr Gln Ile
50 55 60

Ala Tyr Ser Leu Ile Glu Glu Gln Glu Gly Arg Arg Arg Pro Leu Asp
65 70 75 80

Asp Tyr Ile Ser Phe Val Ser Leu Leu Ala Asp Pro Arg Tyr Cys Gly
85 90 95

Ile Ser Tyr Glu Glu Lys Glu Glu Val Arg Val Leu Met Arg Gln Asp
100 105 110

Pro Lys Phe Trp Thr Tyr Arg Pro Met Thr Glu Leu Met Ile Arg Ala
115 120 125

Ala Ala Asp Asp Val Arg Phe Leu Leu Tyr Leu Tyr His Lys Met Met
130 135 140

Gly Lys Leu Asn Gln Arg Ser Leu Trp His Leu Ala Val Arg Gly Ala
145 150 155 160

Leu Tyr Cys Arg Cys Leu Cys Cys Met Asn Asp Ala Asp Phe Ala Asp
165 170 175

Trp Pro Thr Val Pro Pro Ile Pro Val Phe Leu Val Lys Val Val Tyr
180 185 190

Ala Val Glu Thr Lys Lys Arg Arg Val Thr Leu Ala Ser Ile Gly
195 200 205

Leu Leu Ile Val Val Gly Leu Leu Asn Val Ala Asp Asn Leu Lys Ser
210 215 220

Glu Asp Gln Cys Leu Glu Glu Ile Leu Ser Val Leu Asp Val Pro
225 230 235 240

Pro Gly Lys Met Gly Arg Val Ile Gly Arg Lys Gly Ala Ser Ile Leu
245 250 255

Ala Ile Lys Glu Ala Cys Asn Ala Glu Ile Leu Ile Gly Gly Ala Lys
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35 40 45

Arg Leu Arg Ser Ser His Pro Leu Val Val Gly Leu Asp Val Gln Trp
50 55 60

Thr Pro Gly Gly Ser Asp Pro Pro Asp Ile Leu Gln Leu Cys Val
65 70 75 80

Gly Asn Arg Cys Leu Ile Ile Gln Leu Ser His Cys Lys Arg Ile Pro
85 90 95

Glu Val Leu Arg Ser Phe Leu Glu Asp Glu Thr Ile Thr Phe Val Gly
100 105 110

Val Trp Asn Ser Gln Asp Gln Gly Lys Leu Glu Arg Phe Arg His Gln
115 120 125

Leu Glu Ile Trp Arg Leu Leu Asp Ile Arg His Tyr Leu Pro Thr Arg
130 135 140

Leu Leu Asn Ser Ser Phe Glu Lys Ile Val Glu Glu Cys Leu Gly Tyr
145 150 155 160

Lys Gly Val Arg Lys Asp Lys Glu Ile Cys Met Ser Asn Trp Gly Ala
165 170 175

Arg Ser Leu Ser His Asp Gln Ile Val Gln Ala Ser Asp Asp Val Tyr
180 185 190

Val Cys Cys Lys Leu Gly Val Lys Glu Cys Ile Trp Lys Glu Arg Ser
195 200 205

Asn Val Lys Glu Arg Ile Trp Lys Glu Ser Ser Asn Val Lys Glu His
210 215 220

Ile Trp Lys Glu Ser Ser Lys Leu Tyr Phe Val Gly Val Cys Phe
225 230 235

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Glu Arg Leu Ile Val Thr Val Thr His Thr Pro Ser Val Ile Arg Arg
35 40 45

Trp Ile His Ser Ile Arg Phe Val Ser Arg Leu Arg Leu Ser His Pro
50 55 60

Leu Val Val Gly Leu Gly Val Gln Trp Thr Pro Arg Gly Ser Asp Pro
65 70 75 80

Pro Pro Asp Ile Leu Gln Leu Cys Val Gly Thr Arg Cys Leu Ile Ile
85 90 95

Gln Leu Ser His Cys Lys Tyr Val Pro Asp Val Leu Arg Ser Phe Leu
100 105 110

Glu Asp Gln Thr Ile Thr Phe Val Gly Val Trp Asn Ser Gln Asp Lys
115 120 125

Asp Lys Leu Glu Arg Phe His His Gln Leu Asp Ile Trp Arg Leu Val
130 135 140

His Ile Arg His Tyr Leu His Pro Leu Leu Ser Ser Ser Phe Glu
145 150 155 160

Thr Ile Val Lys Val Tyr Leu Gly His Glu Gly Val Thr Lys Asp Lys
165 170 175

Glu Leu Cys Met Ser Asn Trp Gly Ala Arg Ser Leu Ser His Asp Gln
180 185 190

Ile Val Gln Ala Ser His Asp Val Tyr Val Cys Cys Lys Leu Gly Val

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Lys Glu Arg Leu Trp Lys Met Gly Ala
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35 40 45

Ala Ile Phe Pro Gln Ser Glu Gln Leu Met Ile Tyr Ala Met Thr Arg
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Ala Ser Lys Ser Gly Leu His Arg Val Val Glu Ile Lys Pro Ser Ile
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Val His Val Phe Asn Leu
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Val Leu Lys Ala Ile Met Asn Gly Pro Glu Ser Glu Arg Glu Arg Lys
35 40 45

Val Arg Ala Lys Asn Arg Glu Phe Phe Asn Glu Asp Tyr Arg Ser Gly

50

55

60

Val Asn Ile Tyr Gly Met Ala Val Asp Met Met Lys Ala Met Pro Asp
65 70 75 80

Arg Gly Lys Thr Ser Gly Gln Ser Leu Ala Val Trp Tyr Leu Glu Asp
85 90 95

Phe Gly Val Trp Leu Lys Glu Ser Gly Gln Glu Thr Glu Leu Arg Gln
100 105 110

Lys Tyr Leu Thr Gly Thr Ile Gln Ile Asn Ala Leu Asp Val Cys Thr
115 120 125

Ile Gly Gln Lys Gln Leu Leu Ser Glu Ile Phe Asp Ile Thr Lys Glu
130 135 140

Lys Phe Thr Glu Asp Ile Thr Gln Leu Leu Asp Ala Ala Ile Lys Lys
145 150 155 160

Gln Asp Phe Ser Val Ala Ala Asp Met Ala Ile Gln Tyr Asn Leu Leu
165 170 175

Arg Asp His His Phe Glu His Leu Val Leu Pro Leu Met Leu Ser Gly
180 185 190

Lys Asp Gln Thr Ala Tyr Lys Leu Ile Ser Asn Asn Glu Arg Met Gln
195 200 205

Gln Gln Leu Val Glu Phe Phe Asp Arg Met Val Gly Ile Ser Val Val
210 215 220

Ala Val Glu Glu Met Leu Lys Pro Tyr Lys Glu Thr Lys Ile Met Thr
225 230 235 240

Ile Pro Met Glu Lys Leu Thr Gly Lys Thr Leu Asp Lys Leu Ile Ser
245 250 255

Thr Ile Ile Asn Lys Asn Thr His Glu Tyr Asn Phe Ser Arg Glu Leu
260 265 270

Ser Lys Phe Ala Lys Asn His Ser Gln Asn Gly Asn Leu Lys Ala Leu
275 280 285

Lys Phe Asn Ile Ser Glu Arg Tyr Glu Lys Gly Lys Ser Asp Asp Asn
290 295 300

Tyr Phe Gln His Met Val Glu Thr Phe Thr Lys Ala Glu Asp Val Arg
305 310 315 320

Glu Pro Ile Leu Phe Tyr Leu Trp Ser Ser Asn Asp Thr Glu Lys Gln
325 330 335

Ile Asp Ala Ile Cys Phe Ala Ile Tyr Leu Gly Ile Ala Ser Ser Ser
340 345 350

Ser Tyr Gln Leu Pro Asn Val Met Arg Asp Phe Phe Arg Gln Pro Asp

355

360

365

Ser Lys Leu Arg Glu Ala Lys Glu Leu Leu Val Arg Arg Lys Thr Leu
370 375 380

Gln Val Pro Leu Asn Gly Glu Gln Leu Phe Val Phe Glu Asn Glu Arg
385 390 395 400

Arg Thr Gln Ile His Met Val Lys Thr Glu Ser Glu Met Asn Tyr Leu
405 410 415

Cys Ser Glu Ile Lys Ser Leu Ser Asp Glu Pro Ala Pro Val Tyr Val
420 425 430

Gly Phe Asp Ser Glu Trp Lys Pro Ser Asn Leu Thr Ala Val His Asp
435 440 445

Ser Lys Ile Ala Ile Ile Gln Leu Phe Phe Lys Asn Cys Val Trp Leu
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Val Asp Cys Val Glu Leu Glu Lys Ala Asn Met Ala Asp Asp Trp Trp
465 470 475 480

Gln Lys Phe Ala Ser Arg Leu Phe Gly Asp Ser Pro Val Lys Val Val
485 490 495

Gly Phe Asp Met Arg Asn Asp Leu Asp Ala Met Ala Thr Ile Pro Ala
500 505 510

Leu Lys Ser Ser Met Lys Ile Glu Asp Thr Lys Asn Ala Phe Asp Leu
515 520 525

Lys Arg Leu Ala Glu Asn Val Cys Asp Ile Asp Met Glu Ile Leu Glu
530 535 540

Leu Pro Lys Lys Thr Phe Lys Leu Ala Asp Leu Thr His Tyr Leu Leu
545 550 555 560

Gly Leu Glu Leu Asp Lys Thr Glu Gln Cys Ser Asn Trp Gln Cys Arg
565 570 575

Pro Leu Arg Lys Lys Gln Ile Val Tyr Ala Ala Leu Asp Ala Val Val
580 585 590

Val Val Glu Thr Phe Lys Lys Ile Leu Ser Ile Val Glu Glu Lys Asn
595 600 605

Lys Asp Ala Asp Ile Glu Lys Ile Val Arg Glu Ser Asn Val Met Ala
610 615 620

Pro Lys Lys Asp Lys Gly His Lys Ser Tyr Arg Lys Leu Lys Thr Ile
625 630 635 640

Pro Trp Leu Glu Leu Tyr Asp Ile Leu Arg Ser His Arg Asn Pro Thr
645 650 655

Arg Ser Pro Gln Arg Pro His Asp Ile Lys Val Ile Val Asp Thr Met

660	665	670
Leu Ile Gly Phe Gly Lys Asn Leu Arg Arg Val Gly Ile Asp Val Ile		
675	680	685
Leu Pro Lys Asp Val Ser Asp Phe Arg Lys Tyr Leu Lys Glu Ile Glu		
690	695	700
Arg Val Gly Gly Glu His Leu Arg His Ile Ile Thr Val Pro Ser Lys		
705	710	715
Ser Tyr Glu Ala Leu Lys Met Asp Tyr Asp Asn Tyr Thr Ile Ala Ile		
725	730	735
Pro Glu Leu Asn Asn Met Ser Pro Val Asp Gln Leu Ile Glu Phe Phe		
740	745	750
Asp Leu Phe Asn Val Asp Ile Arg Pro Glu Asp Val Tyr Pro Arg Cys		
755	760	765
Thr Glu Cys Asn Ser Arg Leu Gln Ile Lys Phe Pro Gly Pro Val Leu		
770	775	780
His Phe Leu His Gln Tyr Cys Val Ile His Val Gln Asn Val Tyr Arg		
785	790	795
Ala Asp Met Ser Glu Phe Pro Leu Glu Trp Trp Asn Arg Met Leu		
805	810	815
His Ile Asn Pro Asp Asp Tyr Asp Gly Val Lys Val Glu Met Ser Arg		
820	825	830
Pro Ser Pro Thr Ser Lys Trp Ile Val Ala Thr Val Pro Thr Gly Cys		
835	840	845
Leu His Ile Thr Arg Gln Thr Ala Leu His Thr Asn Leu Pro Asp Gly		
850	855	860
Ile Glu Val Arg Ile His Lys Val Pro Asp Asp Glu Phe Lys Arg Arg		
865	870	875
Asn Leu Ser Phe Tyr Val Cys Gly Glu Cys Gly Thr Val Ala Cys Asp		
885	890	895
Gly Arg Gly Asn Gln Ala Ser Glu Ser Thr Ser Gln Glu Cys		
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 <211> 4299
 <212> DNA
 <213> Homo sapiens

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<212> PRT
<213> Homo sapiens

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35 40 45

Phe Thr Gly Ser Ile Val Tyr Ser Tyr Asp Ala Ser Asp Cys Ser Phe
50 55 60

Leu Ser Glu Asp Ile Ser Met Ser Leu Ser Asp Gly Asp Val Val Gly
65 70 75 80

Phe Asp Met Glu Trp Pro Pro Leu Tyr Asn Arg Gly Lys Leu Gly Lys
85 90 95

Val Ala Leu Ile Gln Leu Cys Val Ser Glu Ser Lys Cys Tyr Leu Phe
100 105 110

His Val Ser Ser Met Ser Val Phe Pro Gln Gly Leu Lys Met Leu Leu
115 120 125

Glu Asn Lys Ala Val Lys Lys Ala Gly Val Gly Ile Glu Gly Asp Gln
130 135 140

Trp Lys Leu Leu Arg Asp Phe Asp Ile Lys Leu Lys Asn Phe Val Glu
145 150 155 160

Leu Thr Asp Val Ala Asn Lys Lys Leu Lys Cys Thr Glu Thr Trp Ser
165 170 175

Leu Asn Ser Leu Val Lys His Leu Leu Gly Lys Gln Leu Leu Lys Asp
180 185 190

Lys Ser Ile Arg Cys Ser Asn Trp Ser Lys Phe Pro Leu Thr Glu Asp

195

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205

Gln Lys Leu Tyr Ala Ala Thr Asp Ala Tyr Ala Gly Phe Ile Ile Tyr
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Arg Asn Leu Glu Ile Leu Asp Asp Thr Val Gln Arg Phe Ala Ile Asn
225 230 235 240

Lys Glu Glu Glu Ile Leu Ser Asp Met Asn Lys Gln Leu Thr Ser
245 250 255

Ile Ser Glu Glu Val Met Asp Leu Ala Lys His Leu Pro His Ala Phe
260 265 270

Ser Lys Leu Glu Asn Pro Arg Arg Val Ser Ile Leu Leu Lys Asp Ile
275 280 285

Ser Glu Asn Leu Tyr Ser Leu Arg Arg Met Ile Ile Gly Ser Thr Asn
290 295 300

Ile Glu Thr Glu Leu Arg Pro Ser Asn Asn Leu Asn Leu Leu Ser Phe
305 310 315 320

Glu Asp Ser Thr Thr Gly Gly Val Gln Gln Lys Gln Ile Arg Glu His
325 330 335

Glu Val Leu Ile His Val Glu Asp Glu Thr Trp Asp Pro Thr Leu Asp
340 345 350

His Leu Ala Lys His Asp Gly Glu Asp Val Leu Gly Asn Lys Val Glu
355 360 365

Arg Lys Glu Asp Gly Phe Glu Asp Gly Val Glu Asp Asn Lys Leu Lys
370 375 380

Glu Asn Met Glu Arg Ala Cys Leu Met Ser Leu Asp Ile Thr Glu His
385 390 395 400

Glu Leu Gln Ile Leu Glu Gln Gln Ser Gln Glu Glu Tyr Leu Ser Asp
405 410 415

Ile Ala Tyr Lys Ser Thr Glu His Leu Ser Pro Asn Asp Asn Glu Asn
420 425 430

Asp Thr Ser Tyr Val Ile Glu Ser Asp Glu Asp Leu Glu Met Glu Met
435 440 445

Leu Lys His Leu Ser Pro Asn Asp Asn Glu Asn Asp Thr Ser Tyr Val
450 455 460

Ile Glu Ser Asp Glu Asp Leu Glu Met Glu Met Leu Lys Ser Leu Glu
465 470 475 480

Asn Leu Asn Ser Gly Thr Val Glu Pro Thr His Ser Lys Cys Leu Lys
485 490 495

Met Glu Arg Asn Leu Gly Leu Pro Thr Lys Glu Glu Glu Asp Asp

500

505

510

Glu Asn Glu Ala Asn Glu Gly Glu Glu Asp Asp Asp Lys Asp Phe Leu
515 520 525

Trp Pro Ala Pro Asn Glu Glu Gln Val Thr Cys Leu Lys Met Tyr Phe
530 535 540

Gly His Ser Ser Phe Lys Pro Val Gln Trp Lys Val Ile His Ser Val
545 550 555 560

Leu Glu Glu Arg Arg Asp Asn Val Ala Val Met Ala Thr Gly Tyr Gly
565 570 575

Lys Ser Leu Cys Phe Gln Tyr Pro Pro Val Tyr Val Gly Lys Ile Gly
580 585 590

Leu Val Ile Ser Pro Leu Ile Ser Leu Met Glu Asp Gln Val Leu Gln
595 600 605

Leu Lys Met Ser Asn Ile Pro Ala Cys Phe Leu Gly Ser Ala Gln Ser
610 615 620

Glu Asn Val Leu Thr Asp Ile Lys Leu Gly Lys Tyr Arg Ile Val Tyr
625 630 635 640

Val Thr Pro Glu Tyr Cys Ser Gly Asn Met Gly Leu Leu Gln Gln Leu
645 650 655

Glu Ala Asp Ile Gly Ile Thr Leu Ile Ala Val Asp Glu Ala His Cys
660 665 670

Ile Ser Glu Trp Gly His Asp Phe Arg Asp Ser Phe Arg Lys Leu Gly
675 680 685

Ser Leu Lys Thr Ala Leu Pro Met Val Pro Ile Val Ala Leu Thr Ala
690 695 700

Thr Ala Ser Ser Ser Ile Arg Glu Asp Ile Val Arg Cys Leu Asn Leu
705 710 715 720

Arg Asn Pro Gln Ile Thr Cys Thr Gly Phe Asp Arg Pro Asn Leu Tyr
725 730 735

Leu Glu Val Arg Arg Lys Thr Gly Asn Ile Leu Gln Asp Leu Gln Pro
740 745 750

Phe Leu Val Lys Thr Ser Ser His Trp Glu Phe Glu Gly Pro Thr Ile
755 760 765

Ile Tyr Cys Pro Ser Arg Lys Met Thr Gln Gln Val Thr Gly Glu Leu
770 775 780

Arg Lys Leu Asn Leu Ser Cys Gly Thr Tyr His Ala Gly Met Ser Phe
785 790 795 800

Ser Thr Arg Lys Asp Ile His His Arg Phe Val Arg Asp Glu Ile Gln

805 810 815

Cys Val Ile Ala Thr Ile Ala Phe Gly Met Gly Ile Asn Lys Ala Asp
820 825 830

Ile Arg Gln Val Ile His Tyr Gly Ala Pro Lys Asp Met Glu Ser Tyr
835 840 845

Tyr Gln Glu Ile Gly Arg Ala Gly Arg Asp Gly Leu Gln Ser Ser Cys
850 855 860

His Val Leu Trp Ala Pro Ala Asp Ile Asn Leu Asn Arg His Leu Leu
865 870 880

Thr Glu Ile Arg Asn Glu Lys Phe Arg Leu Tyr Lys Leu Lys Met Met
885 890 895

Ala Lys Met Glu Lys Tyr Leu His Ser Ser Arg Cys Arg Arg Gln Ile
900 905 910

Ile Leu Ser His Phe Glu Asp Lys Gln Val Gln Lys Ala Ser Leu Gly
915 920 925

Ile Met Gly Thr Glu Lys Cys Cys Asp Asn Cys Arg Ser Arg Leu Asp
930 935 940

His Cys Tyr Ser Met Asp Asp Ser Glu Asp Thr Ser Trp Asp Phe Gly
945 950 960

Pro Gln Ala Phe Lys Leu Leu Ser Ala Val Asp Ile Leu Gly Glu Lys
965 970 975

Phe Gly Ile Gly Leu Pro Ile Leu Phe Leu Arg Gly Ser Asn Ser Gln
980 985 990

Arg Leu Ala Asp Gln Tyr Arg Arg His Ser Leu Phe Gly Thr Gly Lys
995 1000 1005

Asp Gln Thr Glu Ser Trp Trp Lys Ala Phe Ser Arg Gln Leu Ile Thr
1010 1015 1020

Glu Gly Phe Leu Val Glu Val Ser Arg Tyr Asn Lys Phe Met Lys Ile
1025 1030 1040

Cys Ala Leu Thr Lys Lys Gly Arg Asn Trp Leu His Lys Ala Asn Thr
1045 1050 1055

Glu Ser Gln Ser Leu Ile Leu Gln Ala Asn Glu Glu Leu Cys Pro Lys
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Lys Phe Leu Leu Pro Ser Ser Lys Thr Val Ser Ser Gly Thr Lys Glu
1075 1080 1085

His Cys Tyr Asn Gln Val Pro Val Glu Leu Ser Thr Glu Lys Lys Ser
1090 1095 1100

Asn Leu Glu Lys Leu Tyr Ser Tyr Lys Pro Cys Asp Lys Ile Ser Ser

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Ala Tyr Ser Ser Ser Gln Pro Val Ile Ser Ala Gln Glu Gln Glu Thr
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1265 1270 1275 1280
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Gln Lys Ile Ile Ala Asp Val Ile Arg Asn Pro Pro Val Asn Ser Asp
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Ser Gly Leu Gln Pro Ser Cys Asp Val Asn Lys Arg Arg Cys Phe Pro
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Gly Ser Glu Glu Ile Cys Ser Ser Ser Lys Arg Ser Lys Glu Glu Val
1380 1385 1390
Gly Ile Asn Thr Glu Thr Ser Ser Ala Glu Arg Lys Arg Arg Leu Pro
1395 1400 1405
Val Trp Phe Ala Lys Gly Ser Asp Thr Ser Lys Lys Leu Met Asp Lys

1410

1415

1420

Thr Lys Arg Gly Gly Leu Phe Ser
1425 1430

<210> 19
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 19
cgacatgatc tgatacatcg ttatgccatt 30

<210> 20
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide

<400> 20
catttataaa taacgctgcg gacatctac 29

<210> 21
<211> 1041
<212> DNA
<213> Arabidopsis thaliana

<400> 21
atgttgagt ttttcgcttc aggaggaagg tcggccgacac aagaagctaa tgagccacca 60
gttccgatt acattgtgac ggatccgtt caacttcctg ctgatttcct aaacccttct 120
cctgaaaaga aattggttat cggtttgac tgtgagggtg ttgacctctg ccgacatggg 180
aaactttgtt tcatgcagat tgcattctct aatgcaatat acttggttga tgtcatcgaa 240
ggtgagagg tgattatgaa agcgtgtaa cctgcactcg agtctaatta catcacgaaa 300
gttattcactg attgcaagcg tgacagttag gctctatact tccagtttg gataagattg 360
cacaatgtt tggacactca gattgcttat tctctgattt aagaacaaga agggcggagg 420
agacctctag atgattacat atcgtttgtt tcactcctt cgtatccacg ttactgcgtt 480
atatcctatg aagagaaaaa agaagttcgaa gttctcatgc gccaggaccc aaagttttgg 540
acatacaggc ctatgactga gctcatgatc cgcgcagctg ctgatgatgt ccgcttcctt 600
ctgtatctt atcacaaaaat gatgggaaag ctaaatcagc ggtcactatg gcatcttgca 660
gttcgtggtg ctttgtactg tcgggtgtctc tgctgcatga atgatgctga ttttgcgtat 720
tggccaaccg ttccctcaat tccagttttc ctgcgttaagg tcgttatatgc tgttagagaca 780
aagaaaaaaaaa gacgggtgac attagcttcg attgggttac tgattgttagt tggactttt 840
aatgtggcag ataacctgaa gtcagaagat caatgtctt aagaagagat cctgtcagt 900
cttgatgttc caccaggaaa gatgggacgt gtgattggaa ggaaaggagc atcgatcctc 960
gccattaagg aagcttgcaa cgcgaaatt ctaattggag gggcaaaggg tccacctgat 1020
aagtttagtc ttattccata g 1041

<210> 22
<211> 346
<212> PRT
<213> Arabidopsis thaliana

<400> 22

Met Phe Glu Phe Phe Ala Ser Gly Gly Arg Ser Pro Thr Gln Glu Ala
1 5 10 15

Asn Glu Pro Pro Val Pro Ile Tyr Ile Val Thr Asp Pro Phe Gln Leu
20 25 30

Pro Ala Asp Phe Leu Asn Pro Ser Pro Glu Lys Lys Leu Val Ile Gly
35 40 45

Phe Asp Cys Glu Gly Val Asp Leu Cys Arg His Gly Lys Leu Cys Ile
50 55 60

Met Gln Ile Ala Phe Ser Asn Ala Ile Tyr Leu Val Asp Val Ile Glu
65 70 75 80

Gly Gly Glu Val Ile Met Lys Ala Cys Lys Pro Ala Leu Glu Ser Asn
85 90 95

Tyr Ile Thr Lys Val Ile His Asp Cys Lys Arg Asp Ser Glu Ala Leu
100 105 110

Tyr Phe Gln Phe Gly Ile Arg Leu His Asn Val Val Asp Thr Gln Ile
115 120 125

Ala Tyr Ser Leu Ile Glu Glu Gln Glu Gly Arg Arg Arg Pro Leu Asp
130 135 140

Asp Tyr Ile Ser Phe Val Ser Leu Leu Ala Asp Pro Arg Tyr Cys Gly
145 150 155 160

Ile Ser Tyr Glu Glu Lys Glu Val Arg Val Leu Met Arg Gln Asp
165 170 175

Pro Lys Phe Trp Thr Tyr Arg Pro Met Thr Glu Leu Met Ile Arg Ala
180 185 190

Ala Ala Asp Asp Val Arg Phe Leu Leu Tyr Leu Tyr His Lys Met Met
195 200 205

Gly Lys Leu Asn Gln Arg Ser Leu Trp His Leu Ala Val Arg Gly Ala
210 215 220

Leu Tyr Cys Arg Cys Leu Cys Cys Met Asn Asp Ala Asp Phe Ala Asp
225 230 235 240

Trp Pro Thr Val Pro Pro Ile Pro Val Phe Leu Val Lys Val Val Tyr
245 250 255

Ala Val Glu Thr Lys Lys Arg Arg Val Thr Leu Ala Ser Ile Gly
260 265 270

Leu Leu Ile Val Val Gly Leu Leu Asn Val Ala Asp Asn Leu Lys Ser
275 280 285

Glu Asp Gln Cys Leu Glu Glu Ile Leu Ser Val Leu Asp Val Pro
290 295 300

Pro Gly Lys Met Gly Arg Val Ile Gly Arg Lys Gly Ala Ser Ile Leu
305 310 315 320

Ala Ile Lys Glu Ala Cys Asn Ala Glu Ile Leu Ile Gly Gly Ala Lys
325 330 335

Gly Pro Pro Asp Lys Val Ser Leu Ile Pro
340 345

<210> 23

<211> 1049

<212> DNA

<213> Arabidopsis thaliana

<400> 23

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tcgacgcgc	ttttacagag	gaagagcttc	tcgctatcga	cgccatcgaa	gcttcctaca	120
atttctcccg	ttcttcttct	tcttcttcct	ctgctgctcc	gaccgtacaa	gctacaacct	180
ccgtccatgg	ccacgaggag	gatccaaatc	aaatccccaa	taatatccgt	cgccaaattgc	240
ctcgttccat	cacttcttct	acatcttata	aacgatttcc	tctctccgt	tgccgagcta	300
ggaattttcc	agcaatgagg	tttgggtgta	ggattttgta	tagcaagact	gctactgagg	360
ttgataagcg	agcaatgcag	cttattaaag	ttcttgatac	caagagagat	aatctggaa	420
tagctttgt	tggcttggat	attgagtgg	gaccaagttt	tagaaaagg	gttctccgg	480
ggaagggtgc	gactgtccag	atatgtgtag	atagaatta	ttgtgatgtt	atgcataattt	540
ttcattctgg	tatccctcaa	agtctccaac	atcttattga	agattcaaca	cttgtaaagg	600
tagtattgg	aattgatggt	gactctgtga	agctttcca	tgactatgga	gttagtatca	660
aagatgtga	ggatcttca	gatttagcca	acaaaaaaat	tggtgagat	aaaaaaatggg	720
gccttgcctc	actaactgag	acacttgtt	gcaaagagct	cctgaagcca	aacagaatca	780
ggcttggaa	ctgggagttt	tatccctgt	caaagcagca	gttacaatac	gcagcaacgg	840
atgcttatgc	ttcatggcat	cttacaagg	ttcttaagga	ccttcctgt	gctgtcagtg	900
gctcataacg	tgaaggagga	agcttaaagg	ttagcctata	accccaagag	ttagcatcaa	960
atgatatgt	acacctaatac	tagtcaagta	gatgcaattc	ttgtgaatat	tgtatctagt	1020
tctggccct	ttaaccgtcc	agaaaactag				1049

<210> 24

<211> 288

<212> PRT

<213> Arabidopsis thaliana

<400> 24

Met	Ser	Ser	Ser	Asn	Trp	Ile	Asp	Asp	Ala	Phe	Thr	Glu	Glu	Leu
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Leu	Ala	Ile	Asp	Ala	Ile	Glu	Ala	Ser	Tyr	Asn	Phe	Ser	Arg	Ser	Ser
						20			25			30			

Ser	Ser	Ser	Ser	Ser	Ala	Ala	Pro	Thr	Val	Gln	Ala	Thr	Thr	Ser	Val
					35			40			45				

His Gly His Glu Glu Asp Pro Asn Gln Ile Pro Asn Asn Ile Arg Arg
50 55 60

Gln Leu Pro Arg Ser Ile Thr Ser Ser Thr Ser Tyr Lys Arg Phe Pro
65 70 75 80

Leu Ser Arg Cys Arg Ala Arg Asn Phe Pro Ala Met Arg Phe Gly Gly
85 90 95

Arg Ile Leu Tyr Ser Lys Thr Ala Thr Glu Val Asp Lys Arg Ala Met
100 105 110

Gln Leu Ile Lys Val Leu Asp Thr Lys Arg Asp Glu Ser Gly Ile Ala
115 120 125

Phe Val Gly Leu Asp Ile Glu Trp Arg Pro Ser Phe Arg Lys Gly Val
130 135 140

Leu Pro Gly Lys Val Ala Thr Val Gln Ile Cys Val Asp Ser Asn Tyr
145 150 155 160

Cys Asp Val Met His Ile Phe His Ser Gly Ile Pro Gln Ser Leu Gln
165 170 175

His Leu Ile Glu Asp Ser Thr Leu Val Lys Val Gly Ile Gly Ile Asp
180 185 190

Gly Asp Ser Val Lys Leu Phe His Asp Tyr Gly Val Ser Ile Lys Asp
195 200 205

Val Glu Asp Leu Ser Asp Leu Ala Asn Gln Lys Ile Gly Gly Asp Lys
210 215 220

Lys Trp Gly Leu Ala Ser Leu Thr Glu Thr Leu Val Cys Lys Glu Leu
225 230 235 240

Leu Lys Pro Asn Arg Ile Arg Leu Gly Asn Trp Glu Phe Tyr Pro Leu
245 250 255

Ser Lys Gln Gln Leu Gln Tyr Ala Ala Thr Asp Ala Tyr Ala Ser Trp
260 265 270

His Leu Tyr Lys Val Leu Lys Asp Leu Pro Asp Ala Val Ser Gly Ser
275 280 285

<210> 25
<211> 22
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide

<400> 25
ttcggAACCA ccatcaaaca gg

22

1000
999
998
997
996
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992
991
990

<210> 26
<211> 22
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide

<400> 26
tttgctgcaac tctctcaggg cc 22

<210> 27
<211> 21
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide

<400> 27
tcagctgttg cccgtctcac t 21

<210> 28
<211> 16
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide
Other n=a, c, g, or t

<400> 28
wgtgnagwan canaga 16

<210> 29
<211> 27
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide

<400> 29
gctccggcca cataattcaa acaacac 27

<210> 30
<211> 22
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide

<400> 30
ttcgaaaaca ttacctccga tc 22

<210> 31
<211> 25
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide

<400> 31
ggcttttgca ttggatct actag 25

<210> 32
<211> 25
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide

<400> 32
atgtcatcgt caaattggat cgacg

25

<210> 33
<211> 27
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide

<400> 33
cgcttatcaa cctcagtagc agtcttg

27

<210> 34
<211> 24
<212> DNA
<213> Description of Artificial Sequence:
Oligonucleotide

<400> 34
ttatgagcca ctgacagcat cagg

24

PB/5-31481A

1

3

4

28